

Figure 3 continued

131 GGYELWIKAFLLLVGFWSLLYMMCTLDPSFGAILAAMSLGVFAAFVGTCT 180
228 QHDCNHCAGAFSRNTLVNRLAGWGMDLIGASSTVWEYQHVIGHHQYTNLVS: 276
|||||... ||:|||| ||:|||| ||:|||| ||:||||
181 QHDCNHCAGAFQSRWNKVAGWTLDMIGASGMTWEFQHVLGHHPTYTNLIEE 230
277DTLFLSPENDPDVFSSYPLMRMHPDTAWQPHHRFQHLF 314
|| . |||||.||:|||| . :||||:
231 ENGLQKVSCKMDTKIADQESDDPVSFSTYPMRLHPWHQKRWYHRFQHIY 280
315 APPLFALMTISKVLTSDFAVCLSMKKGSIDCSSRLVPLEGQLLFWGAKLA 364
:| |||.||. | | : | | | | | | | |
281 GPFIFGFMNTINKVVTQDVGVLRLKRLFQIDAECRYASPMYVARFWIMKAL 330
365 NFLQIVLPCYLHGTMGLALFSVAHLVSGEYLAICFIINHISESCEFVN 414
| : ||||: | || ||: || | | | | | | | :
331 TVLYMVALPCYMQGPWHGLKLFALIAHFTCCEVLATMFIVNHIIEGVSYAS 380
415 TSF.....QTAARRTEMLQAAHQ.AEAKK...VKPTPPNDWAVTQ 452
.| | | : | | | | | . | | | |
381 KDAVKGTMAPPKTMHGVTPMNTRKEVEAEASKGAVVKSVPPLDDWAVVQ 430
453 VQCCVNRSGGVLANHLGGGLNHQIEHHLFPSISHANYPTIAPVVKVECE 502
| ||| | || ||||| ||||| : || | | | |
431 CQTSVNVSVGSWFNHFSGGLNHQIEHHLFPGLSHETYYHIQDVFQSTCA 480

Figure 3 continued

503 EYGLPYKNYVTFWDVCGMVQHRLRLMGAPPVPPTNGDKKS* 542
|||.||.. . | | |.:.|||:| . :. |
481 EYGVYPYQHEPSLWTAYWKMLEHLRQLGNEETHESWQRAA* 520